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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/831,426C

DATE: 09/09/2002

TIME: 12:43:31

Input Set : A:\9823seq.txt

Output Set: N:\CRF3\09092002\I831426C.raw

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4 <110> APPLICANT: Hoechst Marion Roussel
5   Bordon-Pallier, F.
6   Rocher, C.
8 <120> TITLE OF INVENTION: Human htFIIIA gene and coded htFIIIA protein
10 <130> FILE REFERENCE: 146.1364
12 <140> CURRENT APPLICATION NUMBER: US 09/831,426C
13 <141> CURRENT FILING DATE: 2001-05-08
15 <160> NUMBER OF SEQ ID NOS: 10
17 <170> SOFTWARE: PatentIn Vers. 2.0
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21 <212> TYPE: DNA
22 <213> ORGANISM: Human
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25 <221> NAME/KEY: CDS
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33 acgtgtctcg gcacgtggca gcgcgcctgg ccctgggctt ggaggcgccg gcgcc ctg 178
34                                     Met
35                                     1
37 gat ccg ccg gcc gtg gtc gcc gag tcg gtg tcg tcc ttg acc atc gcc 226
38 Asp Pro Pro Ala Val Val Ala Glu Ser Val Ser Ser Leu Thr Ile Ala
39           5                10                15
41 gac gcg ttc att gca gcc ggc gag agc tca gct ccg acc ccg ccg cgc 274
42 Asp Ala Phe Ile Ala Ala Gly Glu Ser Ser Ala Pro Thr Pro Pro Arg
43           20                25                30
45 ccc gcg ctt ccc agg agg ttc atc tgc tcc ttc cct gac tgc agc gcc 322
46 Pro Ala Leu Pro Arg Arg Phe Ile Cys Ser Phe Pro Asp Cys Ser Ala
47           35                40                45
49 aat tac agc aaa gcc tgg aag ctt gac gcg cac ctg tgc aag cac acg 370
50 Asn Tyr Ser Lys Ala Trp Lys Leu Asp Ala His Leu Cys Lys His Thr
51           50                55                60                65
53 ggg gag aga cca ttt gtt tgt gac tat gaa ggg tgt ggc aag gcc ttc 418
54 Gly Glu Arg Pro Phe Val Cys Asp Tyr Glu Gly Cys Gly Lys Ala Phe
55           70                75                80
57 atc agg gac tac cat ctg agc cgc cac att ctg act cac aca gga gaa 466
58 Ile Arg Asp Tyr His Leu Ser Arg His Ile Leu Thr His Thr Gly Glu
59           85                90                95
61 aag ccg ttt gtt tgt gca gcc act ggc tgt gat caa aaa ttc aac aca 514
62 Lys Pro Phe Val Cys Ala Ala Thr Gly Cys Asp Gln Lys Phe Asn Thr
63           100               105               110

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65 aaa tca aac ttg aag aaa cat ttt gaa cgc aaa cat gaa aat caa caa 562
66 Lys Ser Asn Leu Lys Lys His Phe Glu Arg Lys His Glu Asn Gln Gln
67 115 120 125
69 aaa caa tat ata tgc agt ttt gaa gac tgt aag aag acc ttt aag aaa 610
70 Lys Gln Tyr Ile Cys Ser Phe Glu Asp Cys Lys Lys Thr Phe Lys Lys
71 130 135 140 145
73 cat cag cag ctg aaa atc cat cag tgc cag cat acc aat gaa cct cta 658
74 His Gln Gln Leu Lys Ile His Gln Cys Gln His Thr Asn Glu Pro Leu
75 150 155 160
77 ttc aag tgt acc cag gaa gga tgt ggg aaa cac ttt gca tca ccc agc 706
78 Phe Lys Cys Thr Gln Glu Gly Cys Gly Lys His Phe Ala Ser Pro Ser
79 165 170 175
81 aag ctg aaa cga cat gcc aag gcc cac gag ggc tat gta tgt caa aaa 754
82 Lys Leu Lys Arg His Ala Lys Ala His Glu Gly Tyr Val Cys Gln Lys
83 180 185 190
85 gga tgt tcc ttt gtg gca aaa aca tgg acg gaa ctt ctg aaa cat gtg 802
86 Gly Cys Ser Phe Val Ala Lys Thr Trp Thr Glu Leu Leu Lys His Val
87 195 200 205
89 aga gaa acc cat aaa gag gaa ata cta tgt gaa gta tgc cgg aaa aca 850
90 Arg Glu Thr His Lys Glu Glu Ile Leu Cys Glu Val Cys Arg Lys Thr
91 210 215 220 225
93 ttt aaa cgc aaa gat tac ctt aag caa cac atg aaa act cat gcc cca 898
94 Phe Lys Arg Lys Asp Tyr Leu Lys Gln His Met Lys Thr His Ala Pro
95 230 235 240
97 gaa agg gat gta tgt cgc tgt cca aga gaa ggc tgt gga aga acc tat 946
98 Glu Arg Asp Val Cys Arg Cys Pro Arg Glu Gly Cys Gly Arg Thr Tyr
99 245 250 255
101 act act gtg ttt aat ctc caa agc cat atc ctc tcc ttc cat gag gaa 994
102 Thr Thr Val Phe Asn Leu Gln Ser His Ile Leu Ser Phe His Glu Glu
103 260 265 270
105 agc cgc cct ttt gtg tgt gaa cat gct ggc tgt ggc aaa aca ttt gca 1042
106 Ser Arg Pro Phe Val Cys Glu His Ala Gly Cys Gly Lys Thr Phe Ala
107 275 280 285
109 atg aaa caa agt ctc act agg cat gct gtt gta cat gat cct gac aag 1090
110 Met Lys Gln Ser Leu Thr Arg His Ala Val Val His Asp Pro Asp Lys
111 290 295 300 305
113 aag aaa atg aag ctc aaa gtc aaa aaa tct cgt gaa aaa cgg agt ttg 1138
114 Lys Lys Met Lys Leu Lys Val Lys Lys Ser Arg Glu Lys Arg Ser Leu
115 310 315 320
117 gcc tct cat ctc agt gga tat atc cct ccc aaa agg aaa caa ggg caa 1186
118 Ala Ser His Leu Ser Gly Tyr Ile Pro Pro Lys Arg Lys Gln Gly Gln
119 325 330 335
121 ggc tta tct ttg tgt caa aac gga gag tca ccc aac tgt gtg gaa gac 1234
122 Gly Leu Ser Leu Cys Gln Asn Gly Glu Ser Pro Asn Cys Val Glu Asp
123 340 345 350
125 aag atg ctc tcg aca gtt gca gta ctt acc ctt ggc taa 1273
126 Lys Met Leu Ser Thr Val Ala Val Leu Thr Leu Gly
127 355 360 365
130 <210> SEQ ID NO: 2

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132 <212> TYPE: PRT
133 <213> ORGANISM: Human
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137 1 5 10 15
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140 20 25 30
142 Arg Pro Ala Leu Pro Arg Arg Phe Ile Cys Ser Phe Pro Asp Cys Ser
143 35 40 45
145 Ala Asn Tyr Ser Lys Ala Trp Lys Leu Asp Ala His Leu Cys Lys His
146 50 55 60
148 Thr Gly Glu Arg Pro Phe Val Cys Asp Tyr Glu Gly Cys Gly Lys Ala
149 65 70 75 80
151 Phe Ile Arg Asp Tyr His Leu Ser Arg His Ile Leu Thr His Thr Gly
152 85 90 95
154 Glu Lys Pro Phe Val Cys Ala Ala Thr Gly Cys Asp Gln Lys Phe Asn
155 100 105 110
157 Thr Lys Ser Asn Leu Lys Lys His Phe Glu Arg Lys His Glu Asn Gln
158 115 120 125
160 Gln Lys Gln Tyr Ile Cys Ser Phe Glu Asp Cys Lys Lys Thr Phe Lys
161 130 135 140
163 Lys His Gln Gln Leu Lys Ile His Gln Cys Gln His Thr Asn Glu Pro
164 145 150 155 160
166 Leu Phe Lys Cys Thr Gln Glu Gly Cys Gly Lys His Phe Ala Ser Pro
167 165 170 175
169 Ser Lys Leu Lys Arg His Ala Lys Ala His Glu Gly Tyr Val Cys Gln
170 180 185 190
172 Lys Gly Cys Ser Phe Val Ala Lys Thr Trp Thr Glu Leu Leu Lys His
173 195 200 205
175 Val Arg Glu Thr His Lys Glu Glu Ile Leu Cys Glu Val Cys Arg Lys
176 210 215 220
178 Thr Phe Lys Arg Lys Asp Tyr Leu Lys Gln His Met Lys Thr His Ala
179 225 230 235 240
181 Pro Glu Arg Asp Val Cys Arg Cys Pro Arg Glu Gly Cys Gly Arg Thr
182 245 250 255
184 Tyr Thr Thr Val Phe Asn Leu Gln Ser His Ile Leu Ser Phe His Glu
185 260 265 270
187 Glu Ser Arg Pro Phe Val Cys Glu His Ala Gly Cys Gly Lys Thr Phe
188 275 280 285
190 Ala Met Lys Gln Ser Leu Thr Arg His Ala Val Val His Asp Pro Asp
191 290 295 300
193 Lys Lys Lys Met Lys Leu Lys Val Lys Lys Ser Arg Glu Lys Arg Ser
194 305 310 315 320
196 Leu Ala Ser His Leu Ser Gly Tyr Ile Pro Pro Lys Arg Lys Gln Gly
197 325 330 335
199 Gln Gly Leu Ser Leu Cys Gln Asn Gly Glu Ser Pro Asn Cys Val Glu
200 340 345 350
202 Asp Lys Met Leu Ser Thr Val Ala Val Leu Thr Leu Gly

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209 <213> ORGANISM: Human
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216 acgtgtctcg gcacgtggca gcgcgcctgg ccctgggctt ggaggcgccg gcgccctgga 180
218 tccgccggcc gtggtcgccg agtcggtgtc gtccctgacc atcgccgacg cgttcattgc 240
220 agccggcgag agctcagctc cgaccccgcc gcgccccgcg cttcccagga ggttcatctg 300
222 ctccctccct gactgcagcg ccaattacag caaagcctgg aagcttgacg cgcacctgtg 360
224 caagcacacg ggggagagac catttgtttg tgactatgaa ggggtgtggc aggccctcat 420
226 cagggactac catctgagcc gccacattct gactcacaca ggagaaaagc cgtttgtttg 480
228 tgcagccact ggctgtgatc aaaaattcaa cacaaaatca aacttgaaga aacattttga 540
230 acgcaaacat gaaaatcaac aaaaacaata tatatgcagt tttgaagact gtaagaagac 600
232 ctttaagaaa catcagcagc tgaaaatcca tcagtgccag cataccaatg aacctctatt 660
234 caagtgtacc caggaaggat gtgggaaaca ctttgcatac ccagcaagc tgaaacgaca 720
236 tgccaaggcc cgcgagggt atgtatgtca aaaaggatgt tcctttgtgg caaaaacatg 780
238 gacggaactt ctgaaacatg tgagagaaac ccataaagag gaaatactat gtgaagtatg 840
240 ccggaaaaca tttaaacgca aagattacct taagcaacac atgaaaactc atgccccaga 900
242 aagggatgta tgtcgtgtc caagagaagg ctgtggaaga acctatacta ctgtgtttaa 960
244 tctccaaagc catatcctct cttccatga ggaaagccgc ccttttgtgt gtgaacatgc 1020
246 tggctgtggc aaaacatttg caatgaaaca aagtctcact aggcattgtg ttgtacatga 1080
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267 tccgccggcc gtggtcgccg agtcggtgtc gtccctgacc atcgccgacg cgttcattgc 180
269 agccggcgag agctcagctc cgaccccgcc gcgccccgcg cttcccagga ggttcatctg 240
271 ctccctccct gactgcagcg ccaattacag caaagcctgg aagcttgacg cgcacctgtg 300
273 caagcacacg ggggagagac catttgtttg tgactatgaa ggggtgtggc aggccctcat 360
275 cagggactac catctgagcc gccacattct gactcacaca ggagaaaagc cgtttgtttg 420
277 tgcagccact ggctgtgatc aaaaattcaa cacaaaatca aacttgaaga aacattttga 480
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281 ctttaagaaa catcagcagc tgaaaatcca tcagtgccag cataccaatg aacctctatt 600
283 caagtgtacc caggaaggat gtgggaaaca ctttgcatac ccagcaagc tgaaacgaca 660
285 tgccaaggcc cgcgagggt atgtatgtca aaaaggatgt tcctttgtgg caaaaacatg 720
287 gacggaactt ctgaaacatg tgagagaaac ccataaagag gaaatactat gtgaagtatg 780
289 ccggaaaaca tttaaacgca aagattacct taagcaacac atgaaaactc atgccccaga 840
291 aagggatgta tgtcgtgtc caagagaagg ctgtggaaga acctatacta ctgtgtttaa 900
293 tctccaaagc catatcctct cttccatga ggaaagccgc ccttttgtgt gtgaacatgc 960

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297 tcctgacaag aagaaaatga agctcaaagt caaaaaatct cgtgaaaaac ggagtttggc 1080
299 ctctcatctc agtgatata tccctcccaa aaggaaacaa gggcaaggct tatctttgtg 1140
301 tcaaaacgga gagtcaccca actgtgtgga agacaagatg ctctcgacag ttgcagtact 1200
303 tacccttggc taa                                     1213
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307 <211> LENGTH: 34
308 <212> TYPE: DNA
309 <213> ORGANISM: Human
311 <400> SEQUENCE: 5
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317 <212> TYPE: DNA
318 <213> ORGANISM: Human
320 <400> SEQUENCE: 6
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354 <213> ORGANISM: Human
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VERIFICATION SUMMARY

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